

**What Is Claimed Is:**

- Claim 1. A method for determining whether a candidate cell is a neuro-endocrine tumor cell, wherein said method comprises the steps of:
- 5 (A) determining the profile of expression of a plurality of genes of said candidate cell; and
- (B) comparing such determined profile of expression with the profile of expression of said genes of a small cell lung cancer cell, a large cell neuroendocrine carcinoma cell, a typical carcinoid tumor cell or an atypical carcinoid tumor cell;
- 10 to thereby determine whether said candidate cell is a neuroendocrine tumor cell.
- Claim 2. The method of claim 1, wherein said method additionally permits a determination of neuroendocrine tumor cell type.
- Claim 3. The method of claim 2, wherein said method determines whether said
- 15 candidate cell is a small cell lung cancer (SCLC) neuroendocrine tumor cell.
- Claim 4. The method of claim 1, wherein said plurality of genes includes one or more genes selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2,
- 20 PTK6, APRT, ARF4L, ARHGDIA, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1, GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCR1, SIP2-28, SIVA, SURF 1, TADA3L, TKI, TYMSTR, and VATI.
- 25 Claim 5. The method of claim 4, wherein said plurality of genes includes one or more genes selected from the group consisting of GGH and CPE.

- Claim 6. The method of claim 2, wherein said method determines whether said candidate cell is a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell.
- Claim 7. The method of claim 2, wherein said method determines whether said candidate cell is a typical carcinoid (TC) neuroendocrine tumor cell.
- Claim 8. The method of claim 2, wherein said method determines whether said candidate cell is an atypical carcinoid (AC) neuroendocrine tumor cell.
- Claim 9. The method of claim 2, wherein said step (A) comprises incubating RNA of said candidate cell, or DNA or RNA amplified from such RNA, in the presence of a plurality of genes, or fragments or RNA transcripts thereof, under conditions sufficient to cause RNA to hybridize to complementary DNA or RNA molecules; and detecting hybridization that occurs.
- Claim 10. The method of claim 9, wherein said plurality of genes, or polynucleotide fragments or RNA transcripts thereof, are distinguishably arrayed in a microarray.
- Claim 11. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in neuroendocrine tumor cells relative to normal cells.
- Claim 12. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells.
- Claim 13. The method of claim 12, wherein said arrayed genes, or polynucleotide fragments or RNA transcripts thereof, include one or more genes

selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGD1A, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1, GCN1L1, 5 GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCR1, SIP2-28, SIVA, SURF 1, TADA3L, TKI, TYMSTR, and VATI, or a polynucleotide fragment or RNA transcript thereof.

10 Claim 14. The method of claim 13, wherein said arrayed genes, or polynucleotide fragments or RNA transcripts thereof, includes one or more genes selected from the group consisting of GGH and CPE, or a polynucleotide fragment or RNA transcript thereof.

15 Claim 15. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to typical carcinoid (TC) neuroendocrine tumor cells.

20 Claim 16. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in small cell lung cancer (SCLC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

25 Claim 17. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells relative to typical carcinoid (TC) neuroendocrine tumor cells.

5 Claim 18. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

Claim 19. The method of claim 10, wherein said microarray comprises arrayed genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in typical carcinoid (TC) neuroendocrine tumor cells relative to atypical carcinoid (AC) neuroendocrine tumor cells.

10 Claim 20. A microarray of genes, or polynucleotide fragments or RNA transcripts thereof for distinguishing a neuroendocrine tumor cell, said microarray comprising a solid support having greater than 10 genes, or  
15 polynucleotide fragments or RNA transcripts thereof, distinguishably arrayed in spaced apart regions, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) cell, a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell, a typical carcinoid (TC) neuroendocrine tumor cell, or an atypical carcinoid (AC) neuroendocrine tumor cell,  
20 relative to a normal cell or a cell belonging to a different neuroendocrine tumor cell type, to permit said microarray to distinguish a neuroendocrine tumor cell.

25 Claim 21. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a neuroendocrine tumor cell relative to a normal cell to permit said microarray to distinguish between a neuroendocrine tumor cell and a normal cell.

Claim 22. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA

transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell.

Claim 23. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

Claim 24. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

Claim 25. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

5 Claim 26. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

10 Claim 27. The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a typical carcinoid (TC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a typical carcinoid (TC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

15 Claim 28. The microarray of claim 20, wherein said genes or polynucleotide fragments or RNA transcripts thereof of said microarray include one or more genes selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGD1A, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1, GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCR1, SIP2-28, SIVA, SURF 1, TADA3L, TKI, TYMSTR, and VAT1, or a polynucleotide fragment or RNA transcript thereof.

25 Claim 29. The method of claim 28, wherein said genes or polynucleotide fragments or RNA transcripts thereof of said microarray include one or more genes selected from the group consisting of GGH and CPE, or a polynucleotide fragment or RNA transcript thereof.